Report

	assembly
# contigs (>= 0 bp)	441
# contigs (>= 1000 bp)	424
# contigs (>= 5000 bp)	333
# contigs (>= 10000 bp)	265
# contigs (>= 25000 bp)	173
# contigs (>= 50000 bp)	138
Total length (>= 0 bp)	62975800
Total length (>= 1000 bp)	62964434
Total length (>= 5000 bp)	62693277
Total length (>= 10000 bp)	62181872
Total length (>= 25000 bp)	60746337
Total length (>= 50000 bp)	59507187
# contigs	441
Largest contig	6789858
Total length	62975800
Reference length	30946587
N50	930943
N75	302430
L50	9
L75	41
# misassemblies	9
# misassembled contigs	5
Misassembled contigs length	13496122
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	405 + 8 part
Unaligned length	31969816
Genome fraction (%)	99.822
Duplication ratio	1.007
# N's per 100 kbp	0.32
# mismatches per 100 kbp	16.63
# indels per 100 kbp	46.91
Largest alignment	6789858
Total aligned length	30996604

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

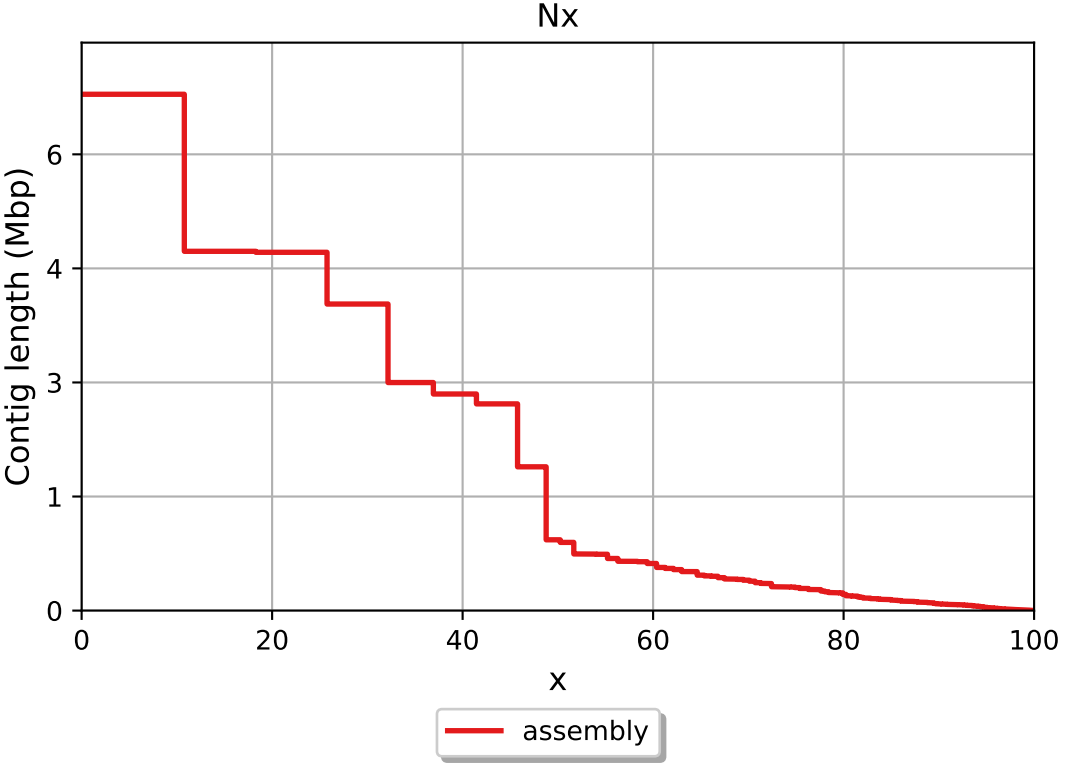
	assembly
# misassemblies	9
# contig misassemblies	9
# c. relocations	5
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	4
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	5
Misassembled contigs length	13496122
# possibly misassembled contigs	7
# possible misassemblies	8
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	5136
# indels	14491
# indels (<= 5 bp)	14451
# indels (> 5 bp)	40
Indels length	16348

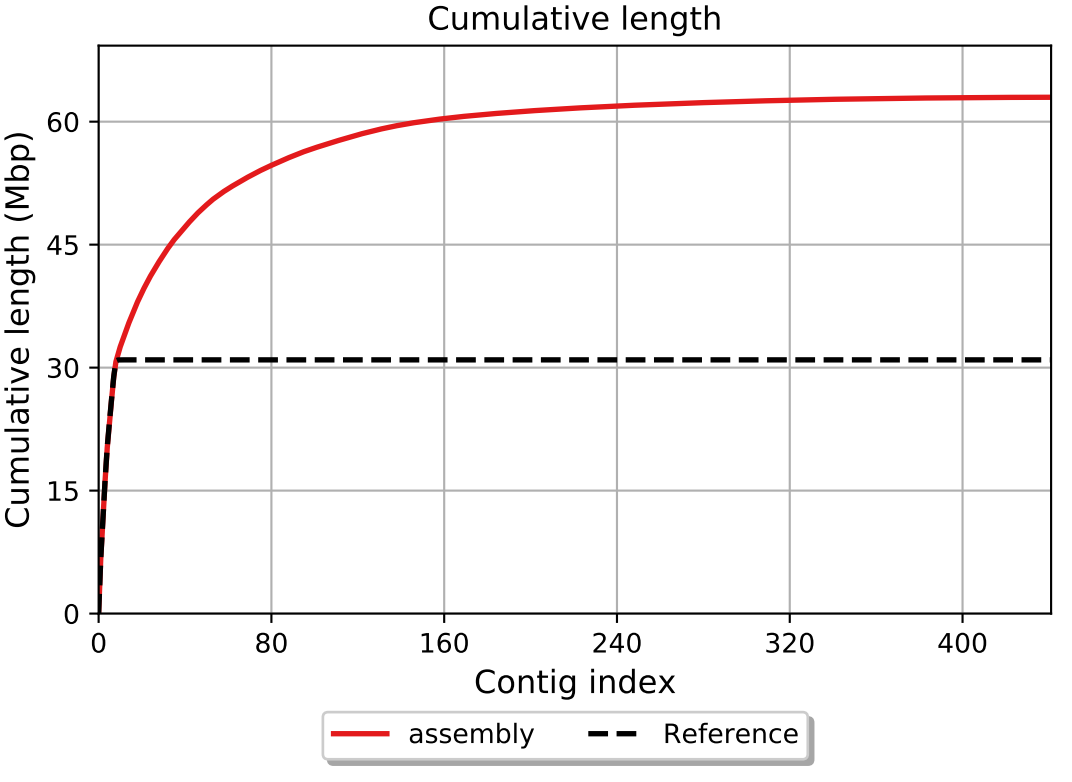
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

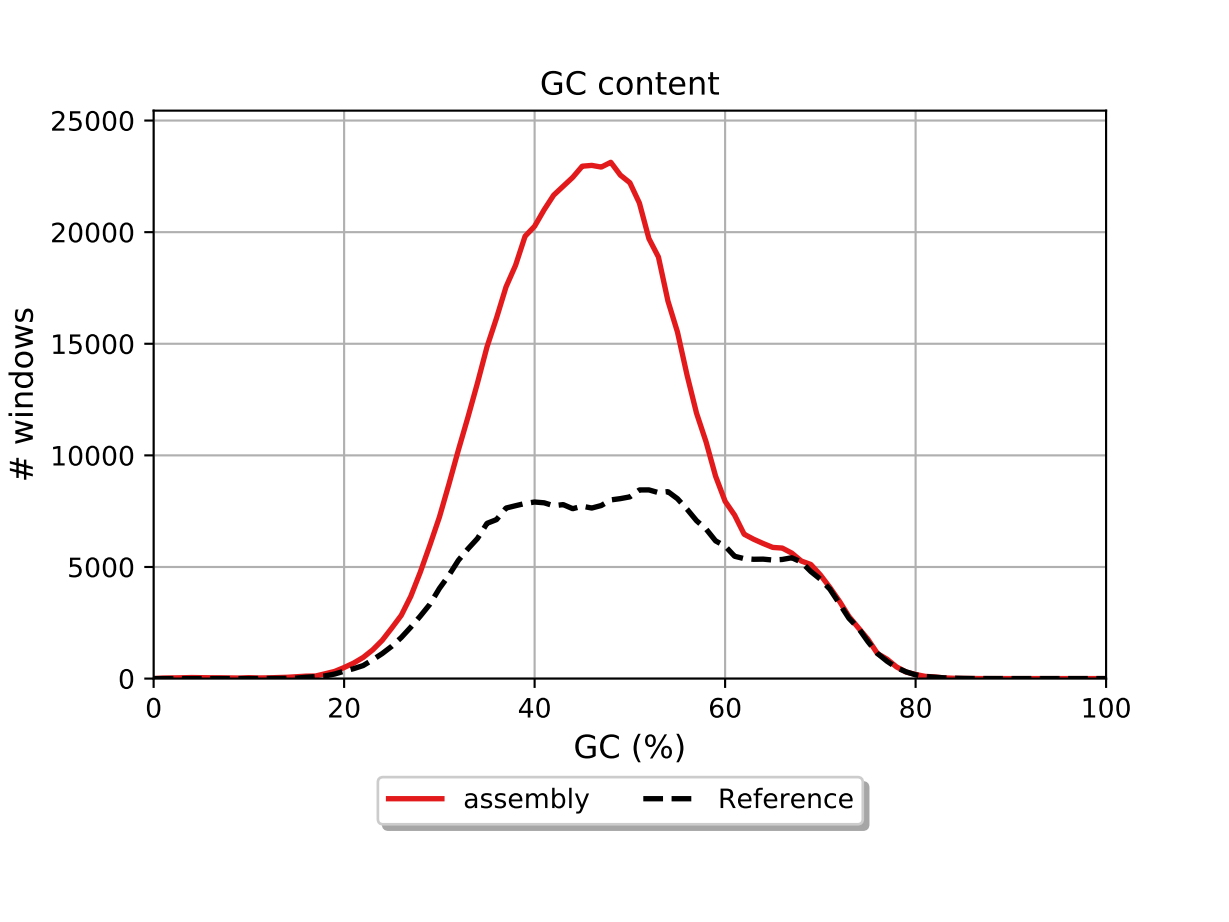
Unaligned report

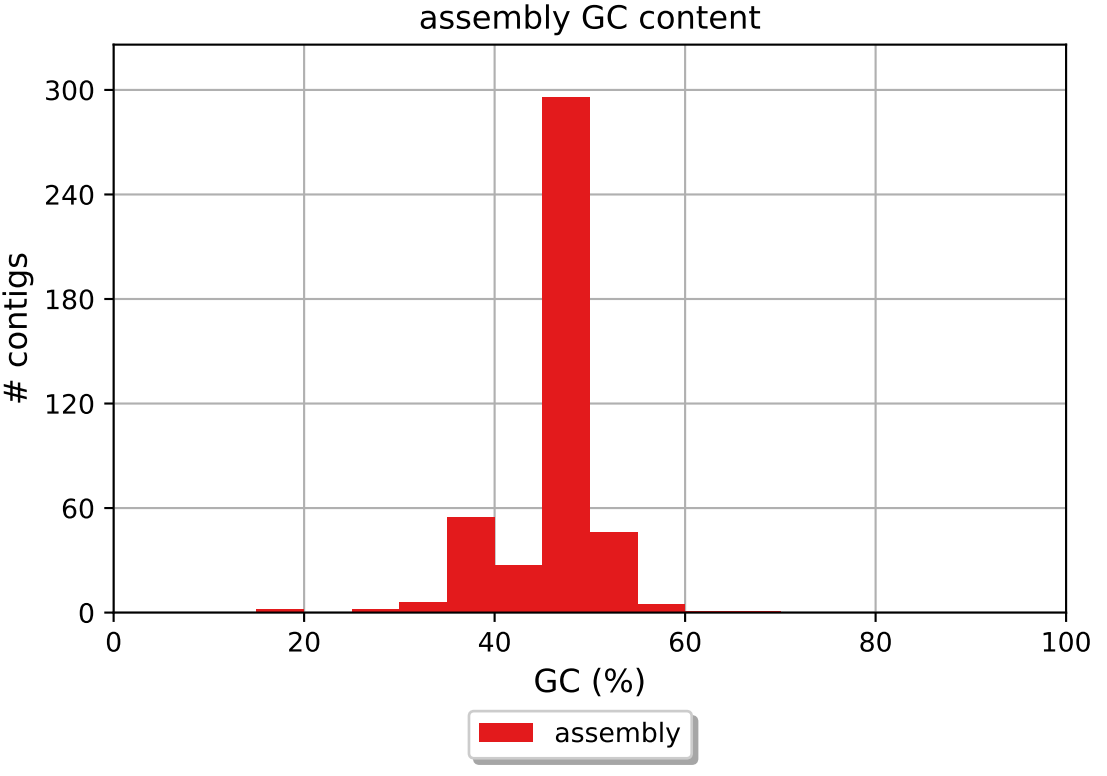
	assembly
# fully unaligned contigs	405
Fully unaligned length	31635527
# partially unaligned contigs	8
Partially unaligned length	334289
# N's	200

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

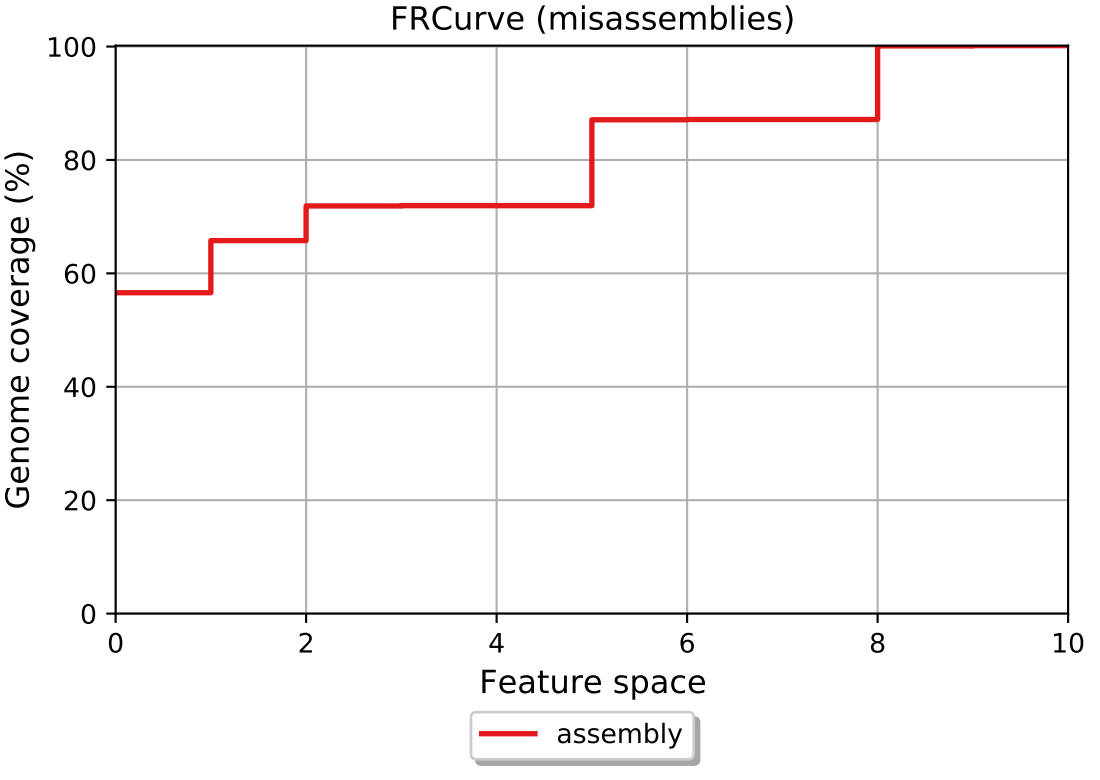

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
assembly

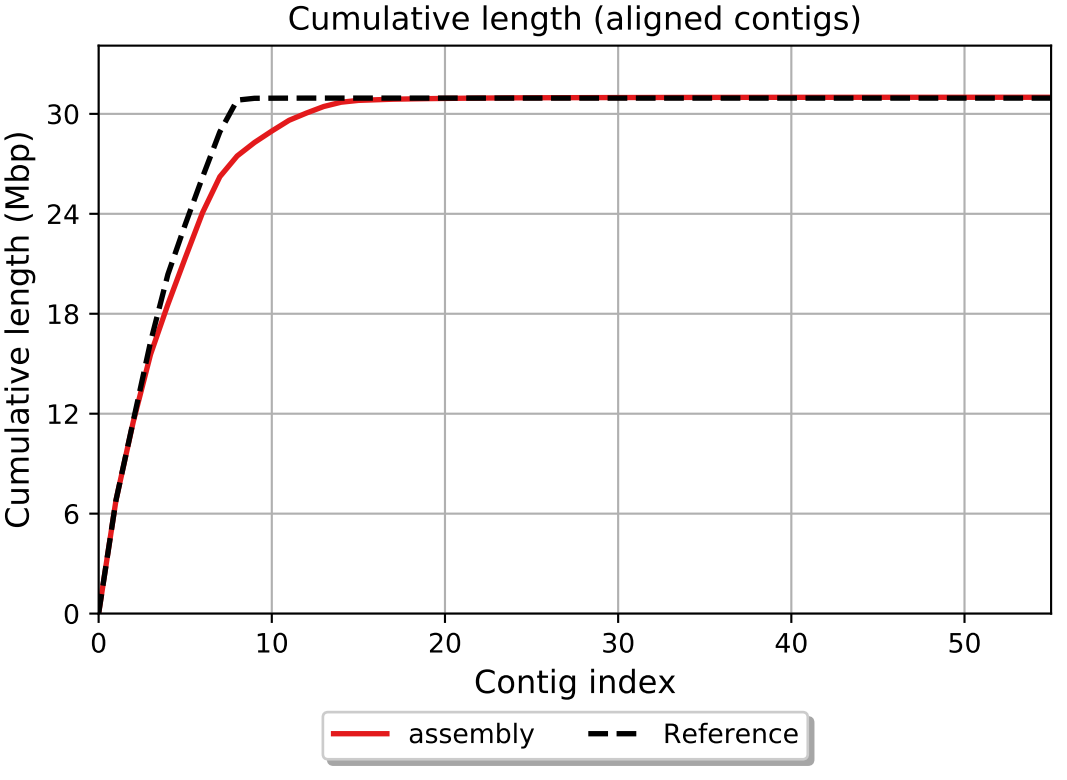

Cumulative length
Cumulative length (Mbp)
0
15
30
45
60
0
80
160
240
320
400
Contig index
assembly
Reference

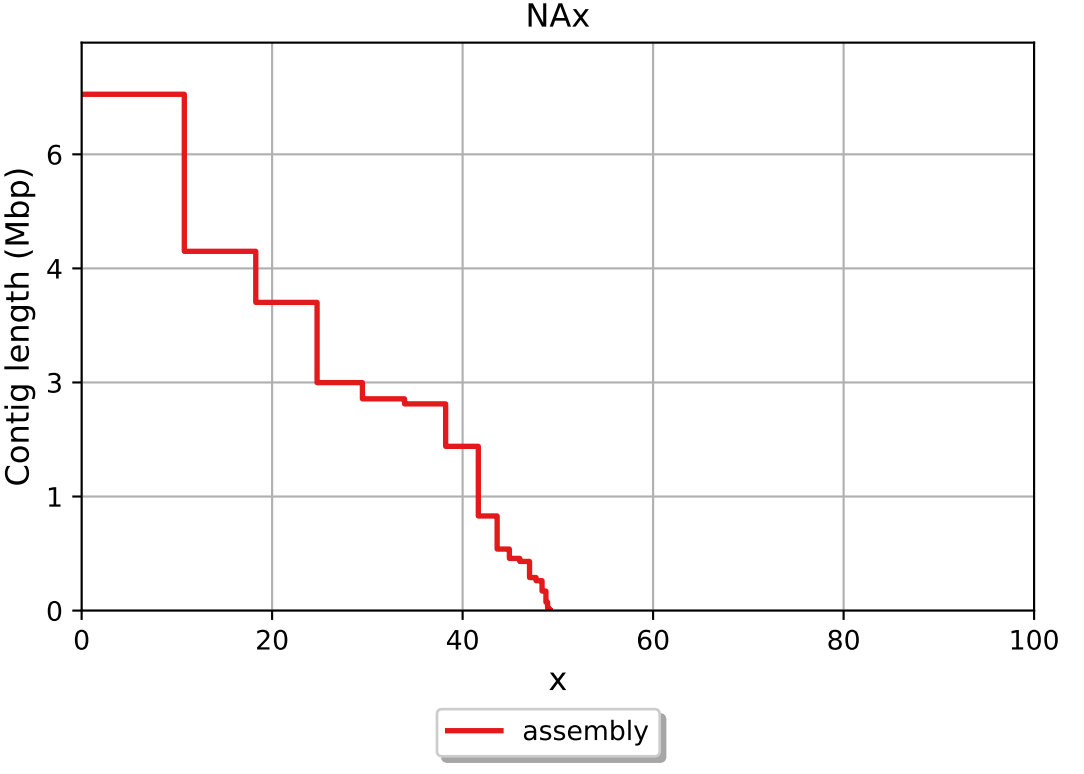

GC content
25000
20000
15000
10000
5000
0
windows
0
20
40
60
80
100
GC (%)
assembly
Reference


assembly GC content
contigs
300
240
180
120
60
0
0
20
40
60
80
100
GC (%)
assembly

Misassemblies
10
8
6
4
2
0
assembly
relocations
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
10
Feature space
assembly


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
6
12
18
24
30
0
10
20
30
40
50
Contig index
assembly
Reference


NAx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
assembly